



IFW16

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/079,241

DATE: 09/09/2004
TIME: 09:49:07

Input Set : A:\Revised sequence listing.txt
Output Set: N:\CRF4\09092004\J079241.raw

3 <110> APPLICANT: Stratagene
 5 <120> TITLE OF INVENTION: HIGH FIDELITY DNA POLYMERASE COMPOSITIONS AND USES THEREFOR
 7 <130> FILE REFERENCE: 25436/2155
 9 <140> CURRENT APPLICATION NUMBER: 10/079,241
 10 <141> CURRENT FILING DATE: 2002-02-20
 12 <160> NUMBER OF SEQ ID NOS: 11
 14 <170> SOFTWARE: PatentIn version 3.1
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 7
 18 <212> TYPE: PRT
 19 <213> ORGANISM: Artificial Sequence
 21 <220> FEATURE:
 22 <223> OTHER INFORMATION: Conserved domain
 24 <220> FEATURE:
 25 <221> NAME/KEY: MISC_FEATURE
 26 <222> LOCATION: (2)..(3)
 27 <223> OTHER INFORMATION: Conserved domain, X at position 2 or 3 is any amino acid.
 30 <400> SEQUENCE: 1
W--> 32 Asp Xaa Xaa Ser Leu Tyr Pro
 33 1 5
 36 <210> SEQ ID NO: 2
 37 <211> LENGTH: 9
 38 <212> TYPE: PRT
 39 <213> ORGANISM: Artificial Sequence
 41 <220> FEATURE:
 42 <223> OTHER INFORMATION: Conserved domain
 44 <220> FEATURE:
 45 <221> NAME/KEY: MISC_FEATURE
 46 <222> LOCATION: (2)..(7)
 47 <223> OTHER INFORMATION: Conserved domain, X at position 2, 3, 4, or 7 is any amino acid.
 50 <400> SEQUENCE: 2
W--> 52 Lys Xaa Xaa Xaa Asn Ser Xaa Tyr Gly
 53 1 5
 56 <210> SEQ ID NO: 3
 57 <211> LENGTH: 5
 58 <212> TYPE: PRT
 59 <213> ORGANISM: Artificial Sequence
 61 <220> FEATURE:
 62 <223> OTHER INFORMATION: Conserved domain
 64 <220> FEATURE:
 65 <221> NAME/KEY: misc_feature
 66 <222> LOCATION: (2)..(3)
 67 <223> OTHER INFORMATION: Conserved domain, X at position 2 or 3 is any amino acid.



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70 <400> SEQUENCE: 3

W--> 72 Thr Xaa Xaa Gly Arg

73 1 5

76 <210> SEQ ID NO: 4

77 <211> LENGTH: 6

78 <212> TYPE: PRT

79 <213> ORGANISM: Artificial Sequence

81 <220> FEATURE:

82 <223> OTHER INFORMATION: Conserved domain

84 <220> FEATURE:

85 <221> NAME/KEY: MISC FEATURE

86 <222> LOCATION: (2)..(2)

87 <223> OTHER INFORMATION: Conserved domain, X at position 2 is any amino acid.

90 <400> SEQUENCE: 4

W--> 92 Tyr Xaa Asp Thr Asp Ser

93 1 5

96 <210> SEQ ID NO: 5

97 <211> LENGTH: 3

98 <212> TYPE: PRT

99 <213> ORGANISM: Artificial Sequence

101 <220> FEATURE:

102 <223> OTHER INFORMATION: Conserved domain

104 <220> FEATURE:

105 <221> NAME/KEY: misc_feature

106 <222> LOCATION: (2)..(2)

107 <223> OTHER INFORMATION: Conserved domain, X at position 2 is any amino acid.

110 <400> SEQUENCE: 5

W--> 112 Lys Xaa Tyr

113 1

116 <210> SEQ ID NO: 6

117 <211> LENGTH: 4

118 <212> TYPE: PRT

119 <213> ORGANISM: Artificial Sequence

121 <220> FEATURE:

122 <223> OTHER INFORMATION: Conserved domain

124 <220> FEATURE:

125 <221> NAME/KEY: MISC FEATURE

126 <222> LOCATION: (2)..(2)

127 <223> OTHER INFORMATION: Conserved domain, X at position 2 is any amino acid.

130 <400> SEQUENCE: 6

W--> 132 Tyr Xaa Gly Gly

133 1

136 <210> SEQ ID NO: 7

137 <211> LENGTH: 6

138 <212> TYPE: PRT

139 <213> ORGANISM: Artificial Sequence

141 <220> FEATURE:

142 <223> OTHER INFORMATION: Conserved domain

144 <220> FEATURE:

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145 <221> NAME/KEY: MISC_FEATURE
 146 <222> LOCATION: (1)..(6)
 147 <223> OTHER INFORMATION: Conserved domain
 150 <400> SEQUENCE: 7
 152 Ser Tyr Thr Gly Gly Phe
 153 1 5
 156 <210> SEQ ID NO: 8
 157 <211> LENGTH: 23
 158 <212> TYPE: DNA
 159 <213> ORGANISM: Artificial Sequence
 161 <220> FEATURE:
 162 <223> OTHER INFORMATION: Synthetic primer
 164 <220> FEATURE:
 165 <221> NAME/KEY: misc_feature
 166 <222> LOCATION: (1)..(23)
 167 <223> OTHER INFORMATION: Synthetic primer
 170 <400> SEQUENCE: 8
 171 gagggagagca ggaaagggtgg aag 23
 174 <210> SEQ ID NO: 9
 175 <211> LENGTH: 23
 176 <212> TYPE: DNA
 177 <213> ORGANISM: Artificial Sequence
 179 <220> FEATURE:
 180 <223> OTHER INFORMATION: Synthetic primer
 182 <220> FEATURE:
 183 <221> NAME/KEY: misc_feature
 184 <222> LOCATION: (1)..(23)
 185 <223> OTHER INFORMATION: Synthetic primer
 188 <400> SEQUENCE: 9
 189 gaggtacagg gttgaggctca ctg 23
 192 <210> SEQ ID NO: 10
 193 <211> LENGTH: 776
 194 <212> TYPE: PRT
 195 <213> ORGANISM: Thermococcus sp. JDF-3
 197 <400> SEQUENCE: 10
 199 Met Ile Leu Asp Val Asp Tyr Ile Thr Glu Asn Gly Lys Pro Val Ile
 200 1 5 10 15
 203 Arg Val Phe Lys Lys Glu Asn Gly Glu Phe Arg Ile Glu Tyr Asp Arg
 204 20 25 30
 207 Glu Phe Glu Pro Tyr Phe Tyr Ala Leu Leu Arg Asp Asp Ser Ala Ile
 208 35 40 45
 211 Glu Glu Ile Lys Lys Ile Thr Ala Glu Arg His Gly Arg Val Val Lys
 212 50 55 60
 215 Val Lys Arg Ala Glu Lys Val Lys Lys Phe Leu Gly Arg Ser Val
 216 65 70 75 80
 219 Glu Val Trp Val Leu Tyr Phe Thr His Pro Gln Asp Val Pro Ala Ile
 220 85 90 95
 223 Arg Asp Lys Ile Arg Lys His Pro Ala Val Ile Asp Ile Tyr Glu Tyr
 224 100 105 110

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227 Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
228 115 120 125
231 Met Glu Gly Glu Glu Leu Lys Leu Met Ser Phe Asp Ile Glu Thr
232 130 135 140
235 Leu Tyr His Glu Gly Glu Glu Phe Gly Thr Gly Pro Ile Leu Met Ile
236 145 150 155 160
239 Ser Tyr Ala Asp Glu Ser Glu Ala Arg Val Ile Thr Trp Lys Lys Ile
240 165 170 175
243 Asp Leu Pro Tyr Val Glu Val Val Ser Thr Glu Lys Glu Met Ile Lys
244 180 185 190
247 Arg Phe Leu Arg Val Val Lys Glu Lys Asp Pro Asp Val Leu Ile Thr
248 195 200 205
251 Tyr Asn Gly Asp Asn Phe Asp Phe Ala Tyr Leu Lys Lys Arg Cys Glu
252 210 215 220
255 Lys Leu Gly Val Ser Phe Thr Leu Gly Arg Asp Gly Ser Glu Pro Lys
256 225 230 235 240
259 Ile Gln Arg Met Gly Asp Arg Phe Ala Val Glu Val Lys Gly Arg Val
260 245 250 255
263 His Phe Asp Leu Tyr Pro Val Ile Arg Arg Thr Ile Asn Leu Pro Thr
264 260 265 270
267 Tyr Thr Leu Glu Ala Val Tyr Glu Ala Val Phe Gly Lys Pro Lys Glu
268 275 280 285
271 Lys Val Tyr Ala Glu Glu Ile Ala Thr Ala Trp Glu Thr Gly Glu Gly
272 290 295 300
275 Leu Glu Arg Val Ala Arg Tyr Ser Met Glu Asp Ala Arg Val Thr Tyr
276 305 310 315 320
279 Glu Leu Gly Arg Glu Phe Phe Pro Met Glu Ala Gln Leu Ser Arg Leu
280 325 330 335
283 Ile Gly Gln Gly Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
284 340 345 350
287 Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
288 355 360 365
291 Pro Asn Lys Pro Asp Glu Arg Glu Leu Ala Arg Arg Arg Gly Tyr
292 370 375 380
295 Ala Gly Gly Tyr Val Lys Glu Pro Glu Arg Gly Leu Trp Asp Asn Ile
296 385 390 395 400
299 Val Tyr Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr His
300 405 410 415
303 Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Arg Ser Tyr Asp
304 420 425 430
307 Val Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly Phe
308 435 440 445
311 Ile Pro Ser Leu Leu Gly Asn Leu Leu Glu Glu Arg Gln Lys Ile Lys
312 450 455 460
315 Arg Lys Met Lys Ala Thr Leu Asp Pro Leu Glu Lys Asn Leu Leu Asp
316 465 470 475 480
319 Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Tyr Tyr Gly Tyr
320 485 490 495
323 Tyr Gly Tyr Ala Arg Ala Arg Trp Tyr Cys Arg Glu Cys Ala Glu Ser

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324	500	505	510
327	Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Met Val Ile Arg Glu Leu		
328	515	520	525
331	Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ala Asp Thr Asp Gly Leu		
332	530	535	540
335	His Ala Thr Ile Pro Gly Ala Asp Ala Glu Thr Val Lys Lys Lys Ala		
336	545	550	555
339	560	565	570
340	Met Glu Phe Leu Asn Tyr Ile Asn Pro Lys Leu Pro Gly Leu Leu Glu		
343	575	580	585
344	Leu Glu Tyr Glu Gly Phe Tyr Val Arg Gly Phe Phe Val Thr Lys Lys		
347	590	595	600
348	Lys Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Thr Thr Arg Gly Leu		
351	605	610	615
352	620	625	630
355	640	635	645
356	Arg Val Leu Glu Ala Ile Leu Arg His Gly Asp Val Glu Glu Ala Val		
359	655	660	665
360	670	675	680
363	Arg Ile Val Arg Glu Val Thr Glu Lys Leu Ser Lys Tyr Glu Val Pro		
364	685	690	695
367	695	700	705
371	Tyr Lys Ala Thr Gly Pro His Val Ala Ile Ala Lys Arg Leu Ala Ala		
372	710	715	720
375	725	730	735
376	735	740	745
379	750	755	760
380	765	770	775
383	775	780	785
384	790	795	800
387	805	810	815
388	820	825	830
391	835	840	845
392	850	855	860
395	<210> SEQ ID NO: 11		
396	<211> LENGTH: 2331		
397	<212> TYPE: DNA		
398	<213> ORGANISM: Thermococcus sp. JDF-3		
400	<400> SEQUENCE: 11		
401	atgatccttg acgttgattt catcaccgag aatggaaagc ccgtcatcag ggtttcaag	60	
403	aaggagaacg gcgagttcag gattgaatac gaccgcgagt tcgagcccta cttctacgcg	120	
405	ctcctcaggc acgactctgc catcgaagaa atcaaaaaga taaccgcgga gaggcacggc	180	
407	agggtcgta aggttaagcg cgccgagaag gtgaagaaaa agttcctcggt caggtctgtg	240	
409	gaggctggg tcctctactt cacgcacccg caggacgttc cggcaatccg cgacaaaata	300	
411	aggaagcacc ccgcggcat cgacatctac gagtacgaca tacccttcgc caagcgctac	360	
413	ctcatagaca agggcctaatt cccgatggaa ggtgaggaag agcttaaact catgtccttc	420	
415	gacatcgaga cgctctacca cgagggagaa gagtttgaa ccggggccgat tctgtatgata	480	
417	agctacgccc atgaaagcga ggcgcgcgtg ataaccctggaa agaagatcga ctttccttac	540	

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/079,241

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Input Set : A:\Revised sequence listing.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 2,3
Seq#:2; Xaa Pos. 2,3,4,7
Seq#:3; Xaa Pos. 2,3
Seq#:4; Xaa Pos. 2
Seq#:5; Xaa Pos. 2
Seq#:6; Xaa Pos. 2

VERIFICATION SUMMARY

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Input Set : A:\Revised sequence listing.txt

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L:32 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:52 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:72 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:92 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:112 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0